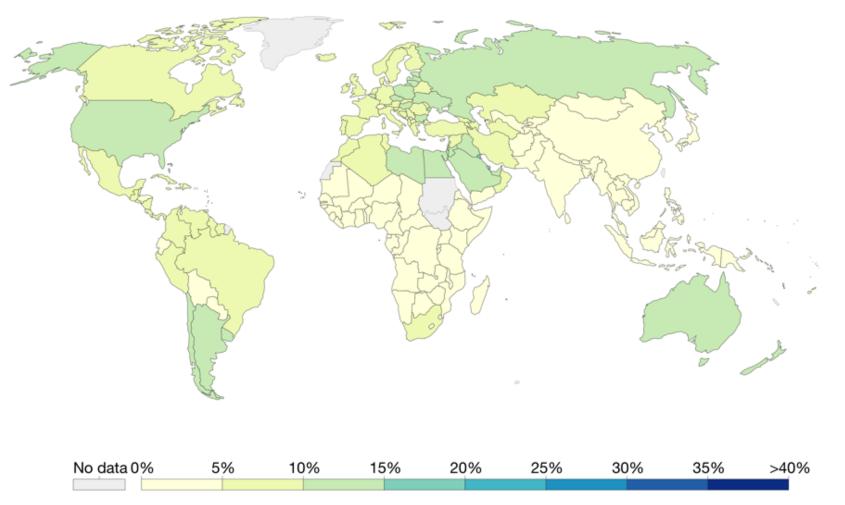
Environmental exposures and mechanisms of transgenerational epigenetic inheritance

To eat or not to eat: Is that the (only) question?

Raquel Chamorro-Garcia Assistant Professor Department of Microbiology and Environmental Toxicology University of California, Santa Cruz

Share of adults that are obese, 1975

Obesity is defined as having a body-mass index (BMI) equal to or greater than 30. BMI is a person's weight in kilograms divided by his or her height in metres squared.



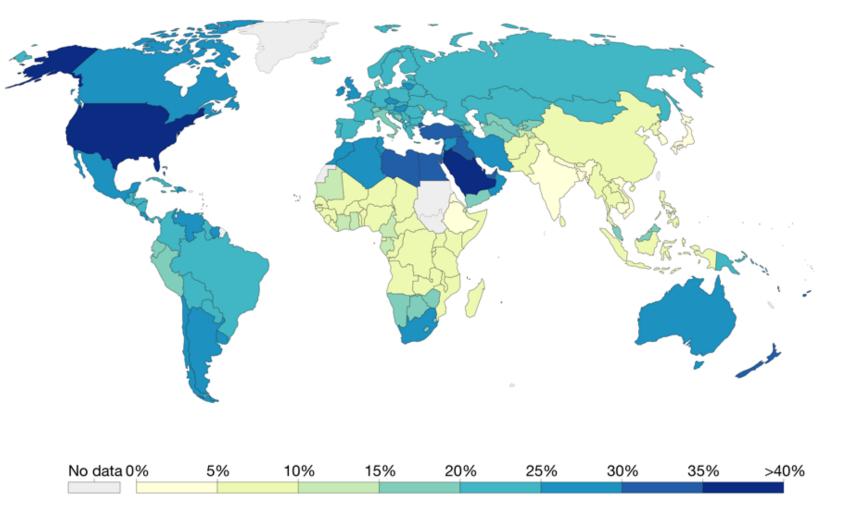
Our World in Data

Source: WHO, Global Health Observatory

OurWorldInData.org/obesity · CC BY

Share of adults that are obese, 2016

Obesity is defined as having a body-mass index (BMI) equal to or greater than 30. BMI is a person's weight in kilograms divided by his or her height in metres squared.



Source: WHO, Global Health Observatory

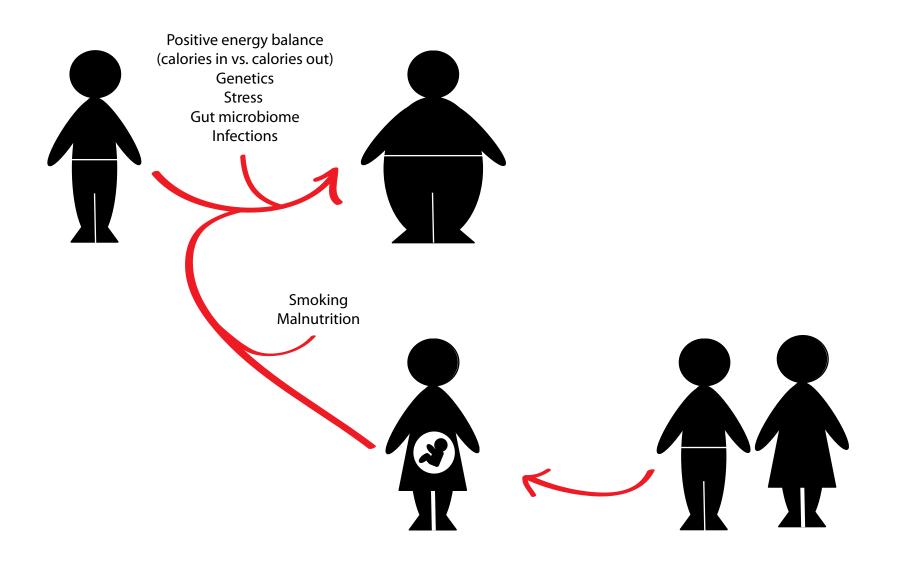
OurWorldInData.org/obesity · CC BY



Global impact of obesity

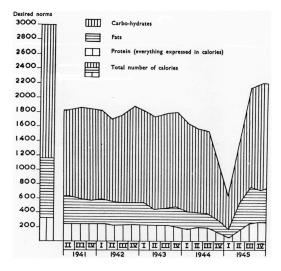


Contributing factors to obesity



Multigenerational studies in humans Dutch famine





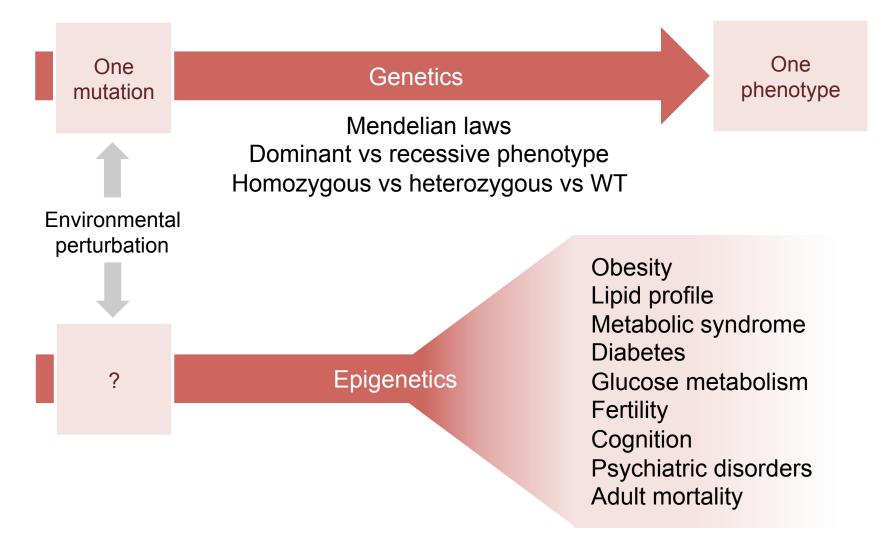
Lumey & Poppel, 2013



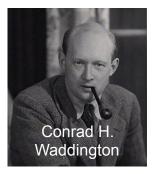
Obesity, lipid profile, metabolic syndrome Diabetes, glucose metabolism Fertility Cognition, psychiatric disorders Adult mortality

Poor health

Multigenerational inheritance

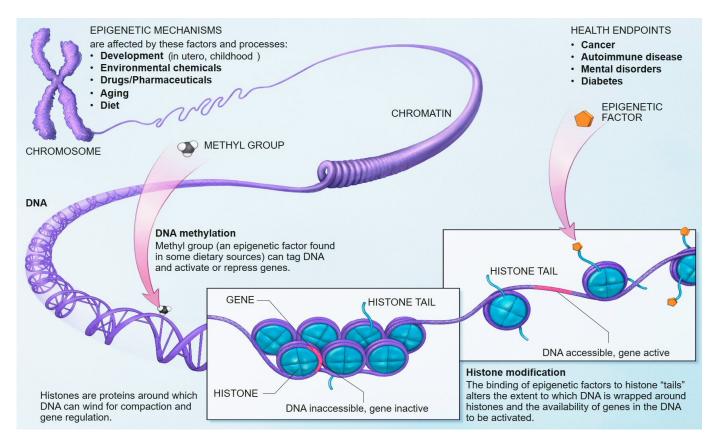


Epigenetics

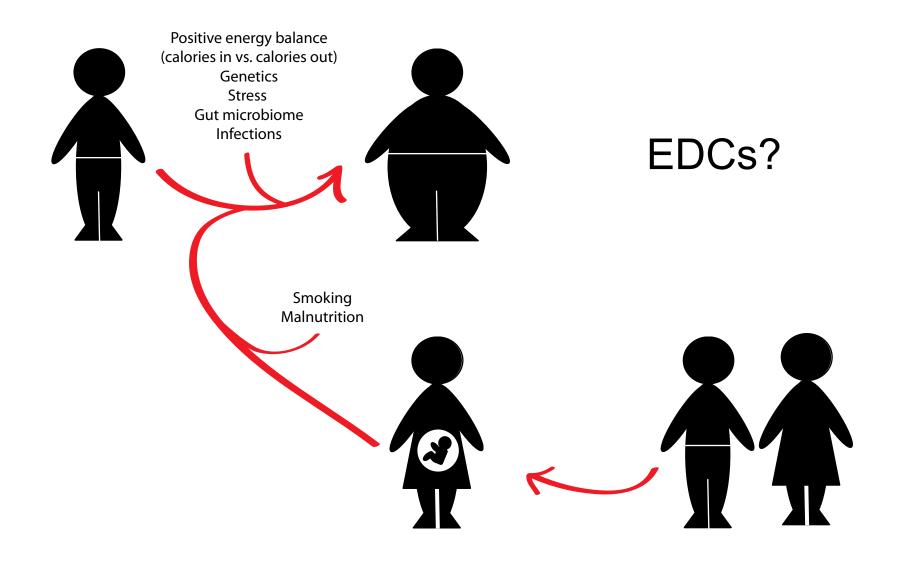


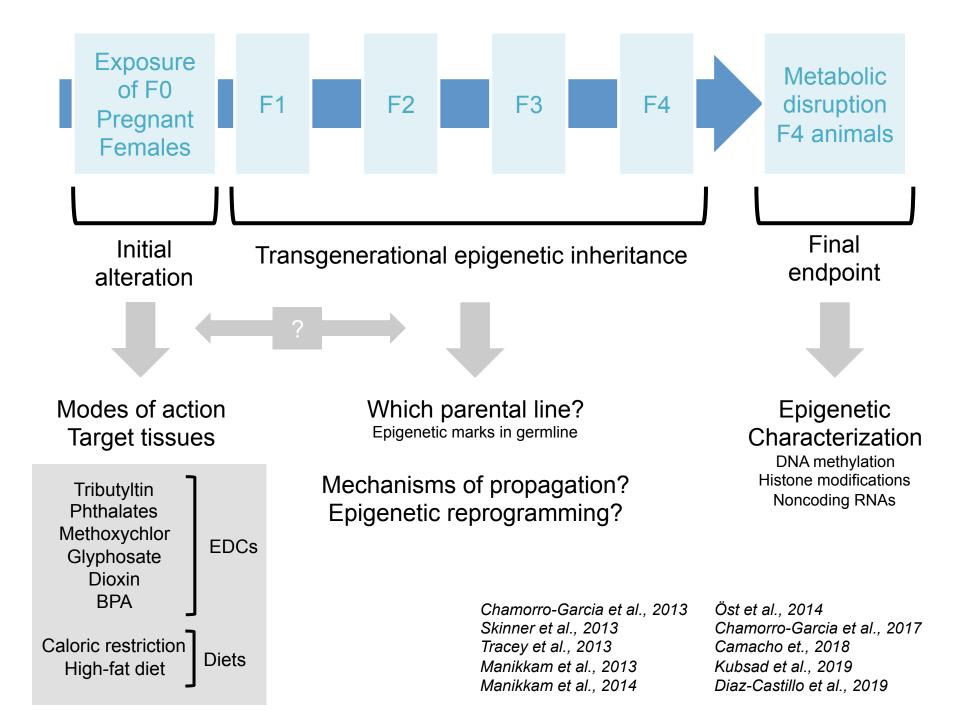
Alterations that lead to a "stably heritable phenotype resulting from changes in a chromosome without alterations in the DNA sequence"

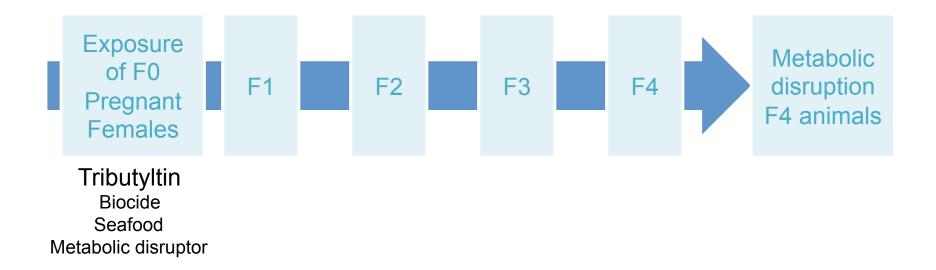
- Cold Spring Harbor Conference, 2008



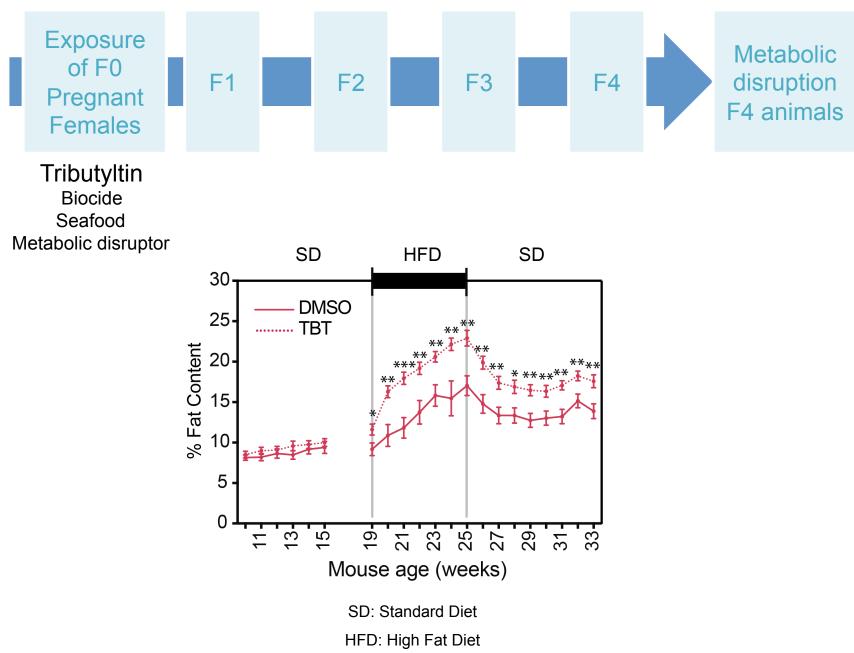
Contributing factors to obesity

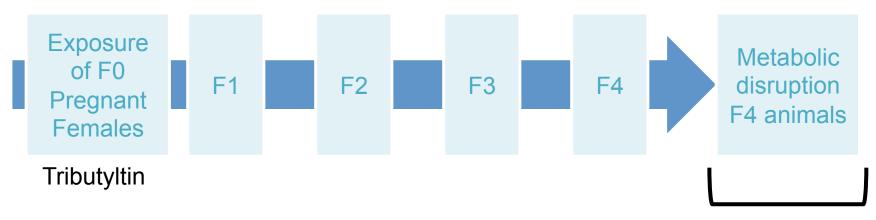










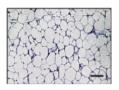


How?

Hypothesis I: TBT alters DNA methylation of promoters for metabolically-relevant genes

Rejected

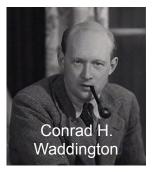
Hypothesis II: TBT alters nuclear genome organization



F4 Adipose tissue

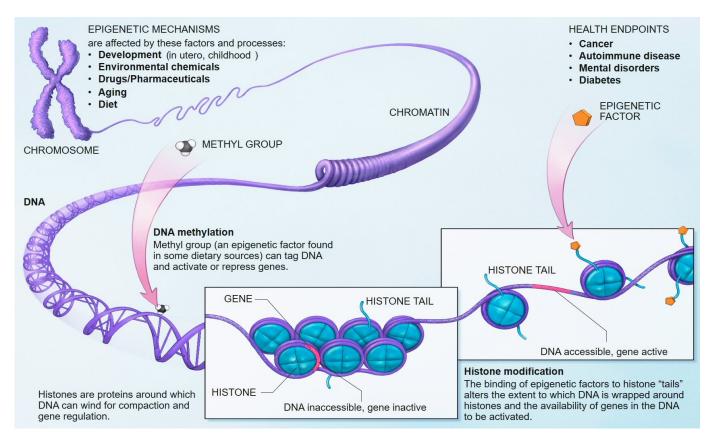
Alterations in methome & transcriptome

Epigenetics



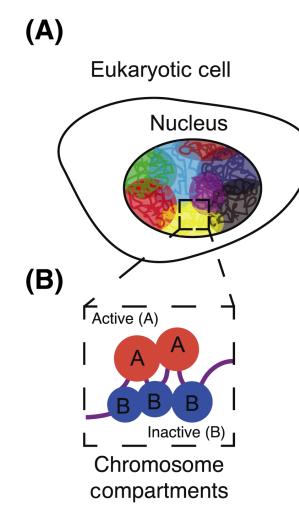
Alterations that lead to a "stably heritable phenotype resulting from changes in a chromosome without alterations in the DNA sequence"

- Cold Spring Harbor Conference, 2008



National Institutes of Health - http://commonfund.nih.gov/epigenomics/figure.aspx

Nuclear genome organization



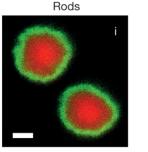
Compartment A

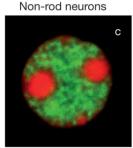
Euchromatin Active genes, Higher accessibility High GC content

Compartment B

Heterochromatin Transcriptionally inactive Less accessible High AT content

Immunofluorescence

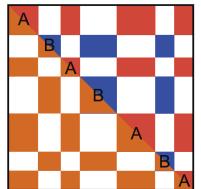




Euchromatin Heterochromatin

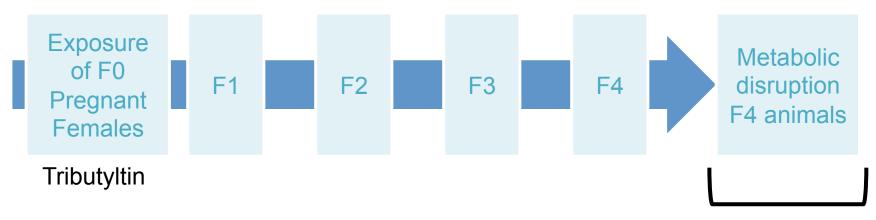
Hi-C





Schematic of compartment signal by Hi-C

Hildebrand & Dekker, 2020 – Trends Biochem Sci Falk et al., 2019 - Nature

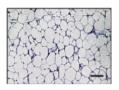


How?

Hypothesis I: TBT alters DNA methylation of promoters for metabolically-relevant genes

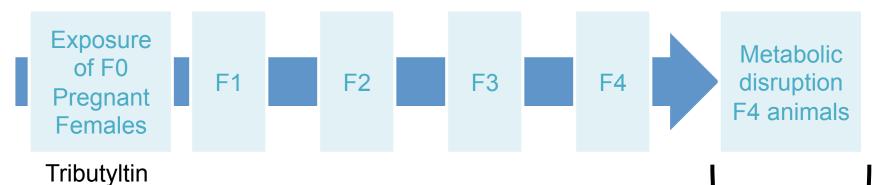
Rejected

Hypothesis II: TBT alters nuclear genome organization



F4 Adipose tissue

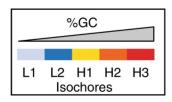
Alterations in methome & transcriptome



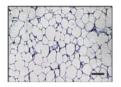
Isochores

- Large regions of DNA (>300 Kb) with highly homogenous base composition (GC- vs. AT-content)
- Reflect multiple levels of organization (TADs, eu-/heterochromatin, compartment A/B)
- Are invariable across tissues, generations and sexes
- Analysis of genomic traits with regards isochores before and after randomly rearranging datasets 10,000 times

Compartment B Heterochromatin AT-enriched Compartment A Euchromatin GC-enriched



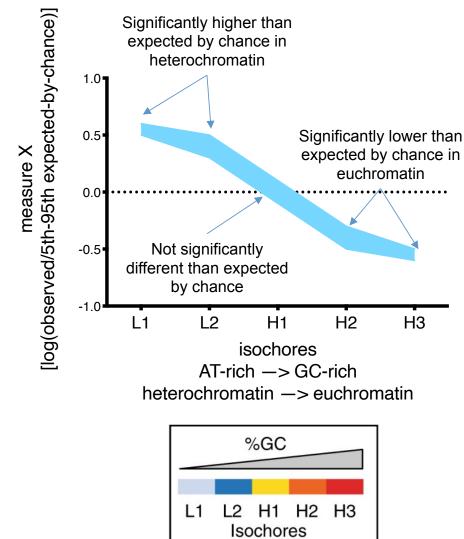
How?

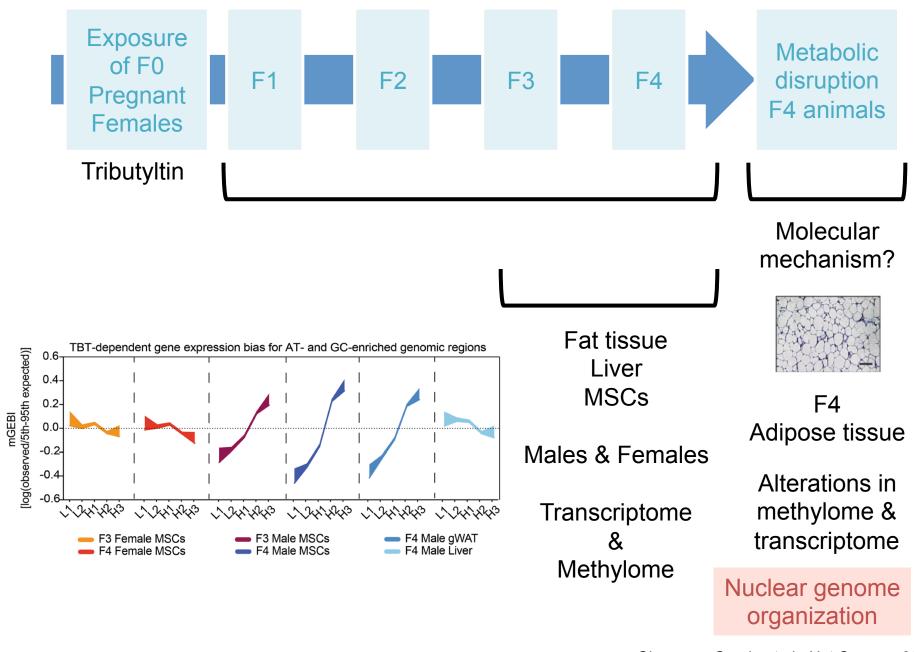


F4 Adipose tissue

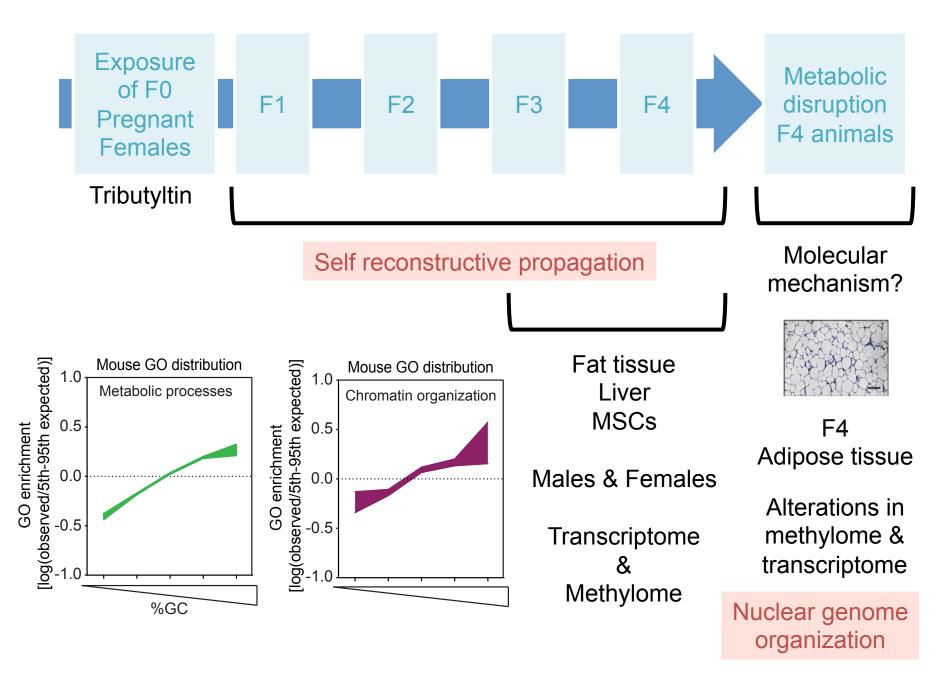
Alterations in methome & transcriptome

Heterochromatin-euchromatin organization disruption TBT vs Control

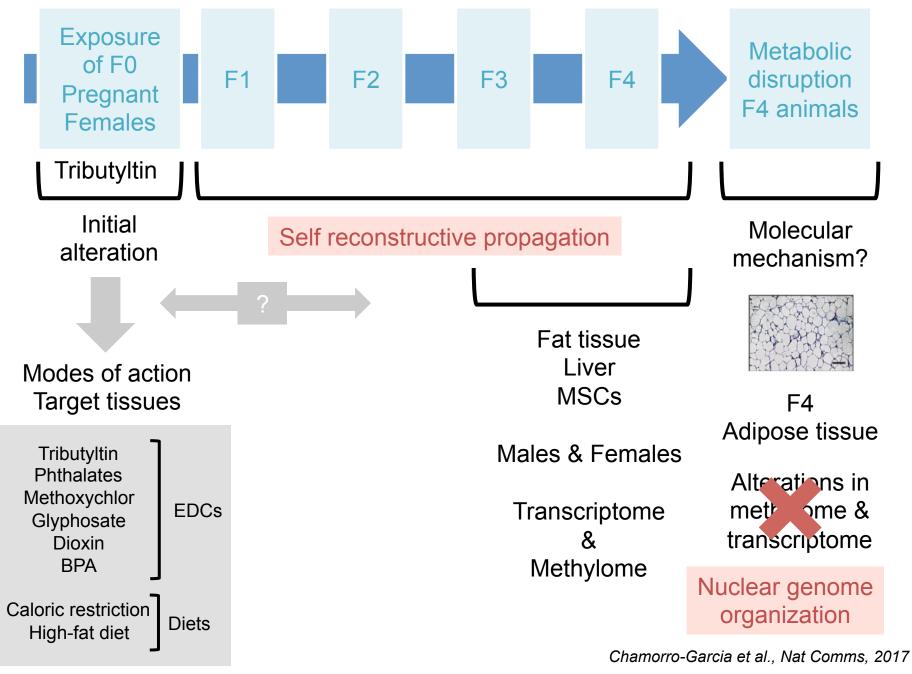




Chamorro-Garcia et al., Nat Comms, 2017 Diaz-Castillo et al., Sci Rep, 2019



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Diaz-Castillo et al., Sci Rep, 2019

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